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(54) **FRAGMENTING DNA SEQUENCES LONGER THAN 10,000 BP USING ULTRASONICATION**

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WO WO9303150 A1 2/1993

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C12Q 1/68 (2006.01)

(52) **U.S. Cl.**

CPC **C12Q 1/6806** (2013.01); **Y10T 436/25**
(2015.01)

(58) **Field of Classification Search**

CPC C12Q 1/6806; C12Q 2523/301; G01N
1/286; B01J 19/10; Y10T 436/25

See application file for complete search history.

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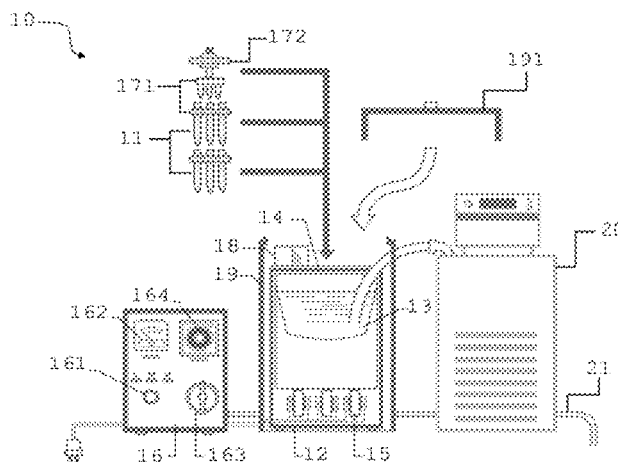
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ABSTRACT

A method of fragmenting a DNA sequence having a starting size of at least 10000 base pair into fragments having a mean size smaller than or equal to 1300 bp, wherein the DNA sequence is put in a solution, the solution comprising the DNA sequence is put in a container and the container is placed in a liquid bath which is subjected to the action of ultrasound waves such that the ultrasound waves travel through the liquid bath to excite the container and the solution so as to shear the DNA sequence, and wherein the ultrasound waves have a frequency falling in the range between 28 kHz and 80 kHz.

20 Claims, 8 Drawing Sheets



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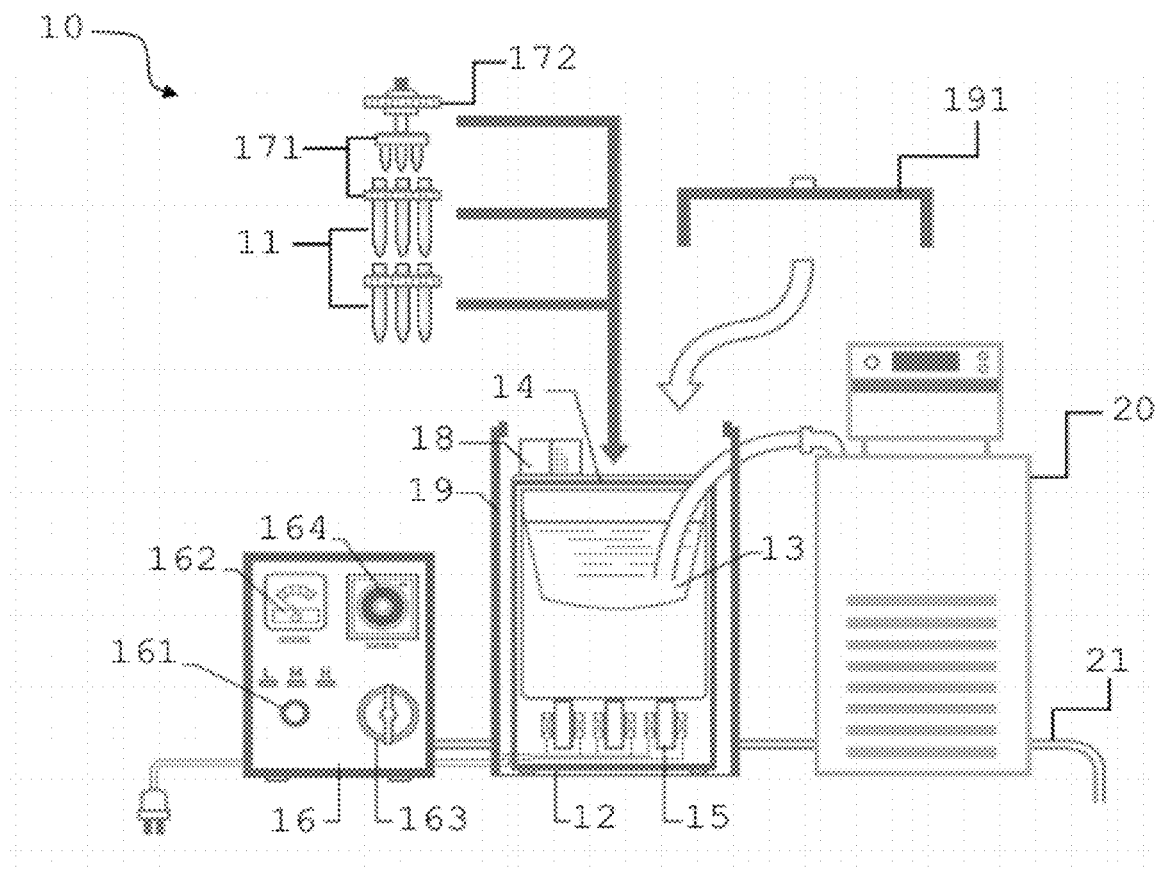


FIG 1

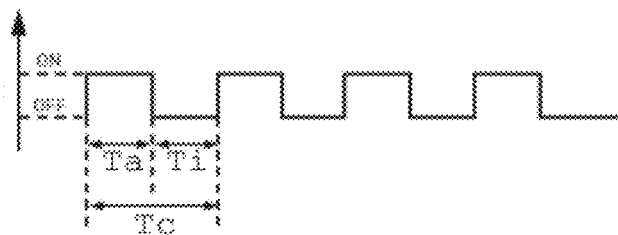


FIG 2

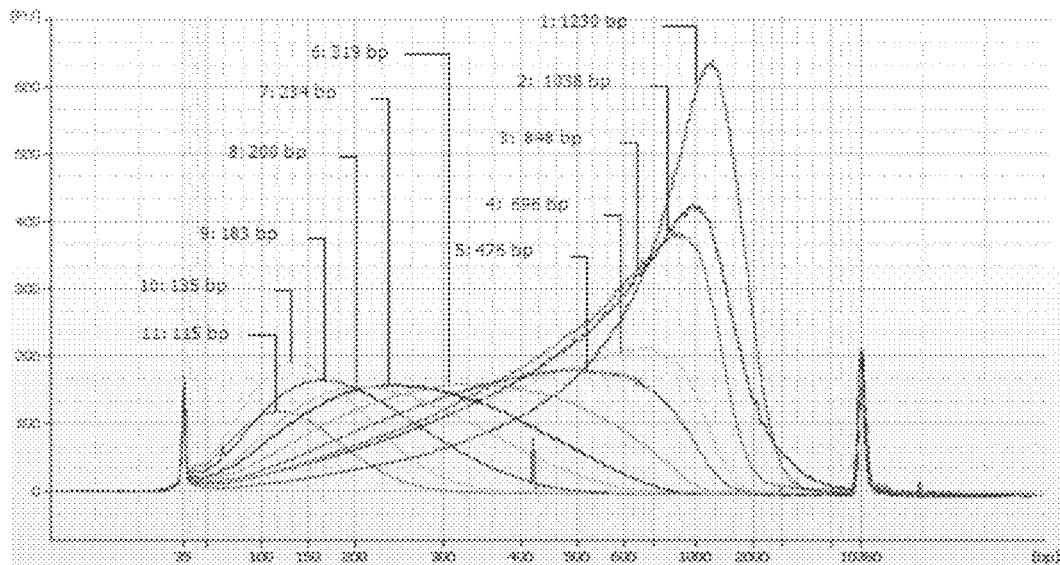
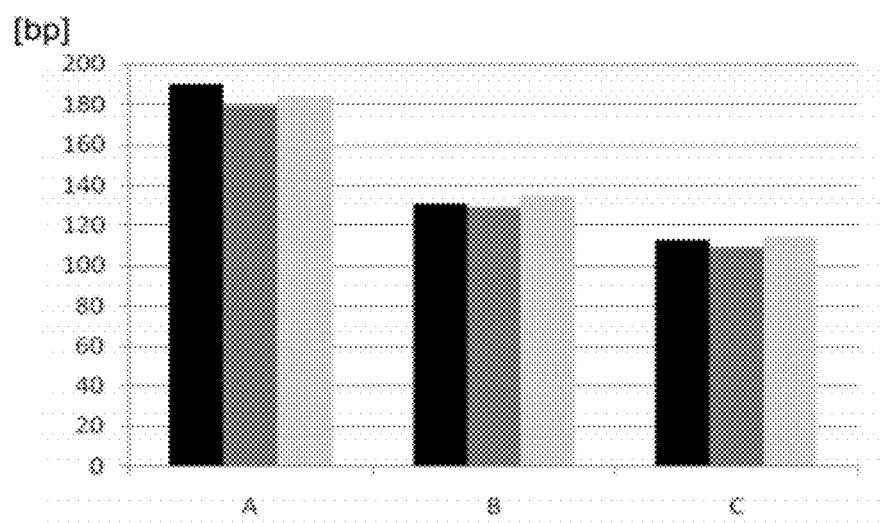
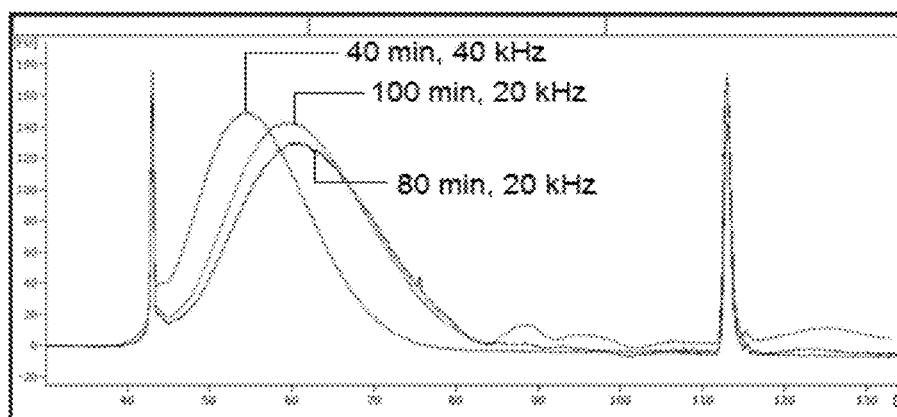
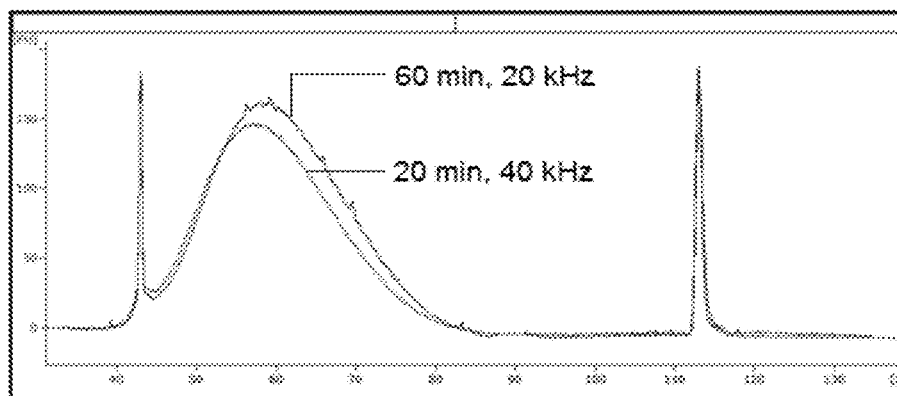
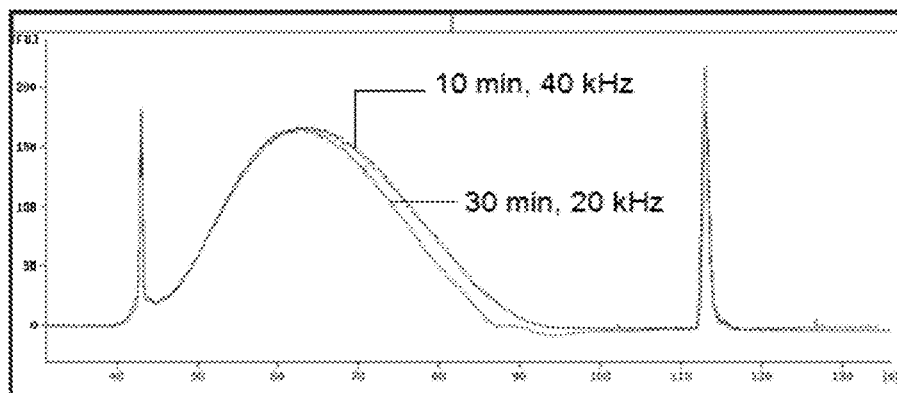
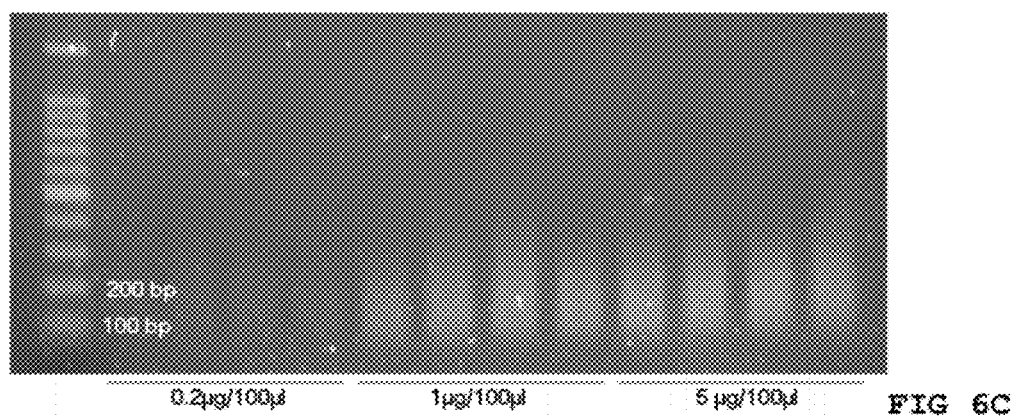
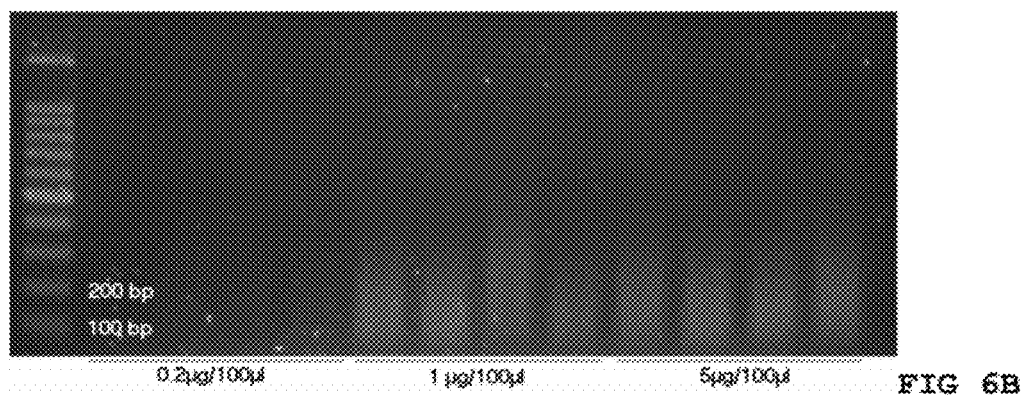
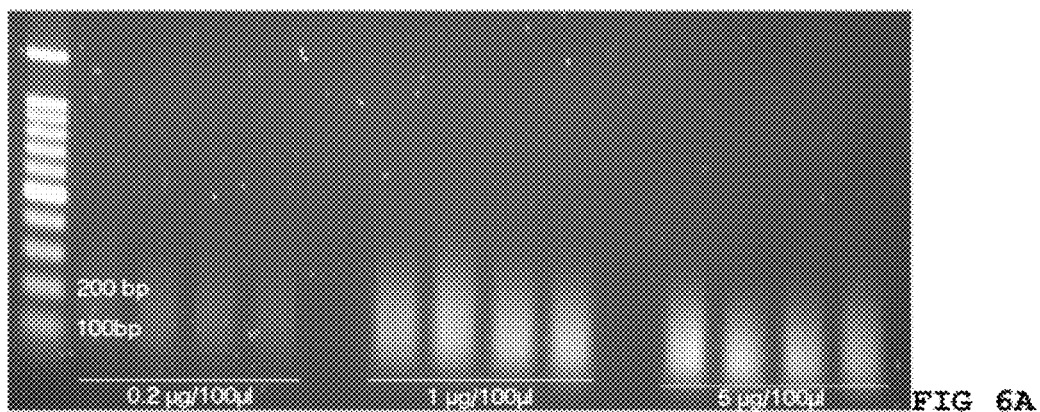


FIG 3

**FIG 4**





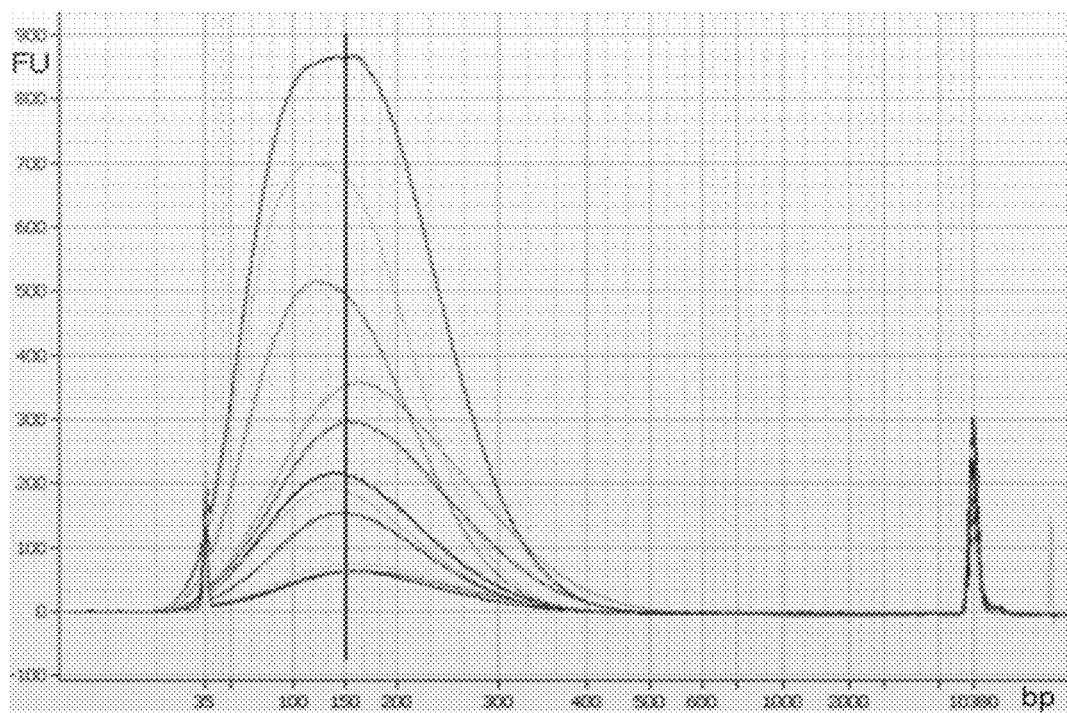


FIG 7

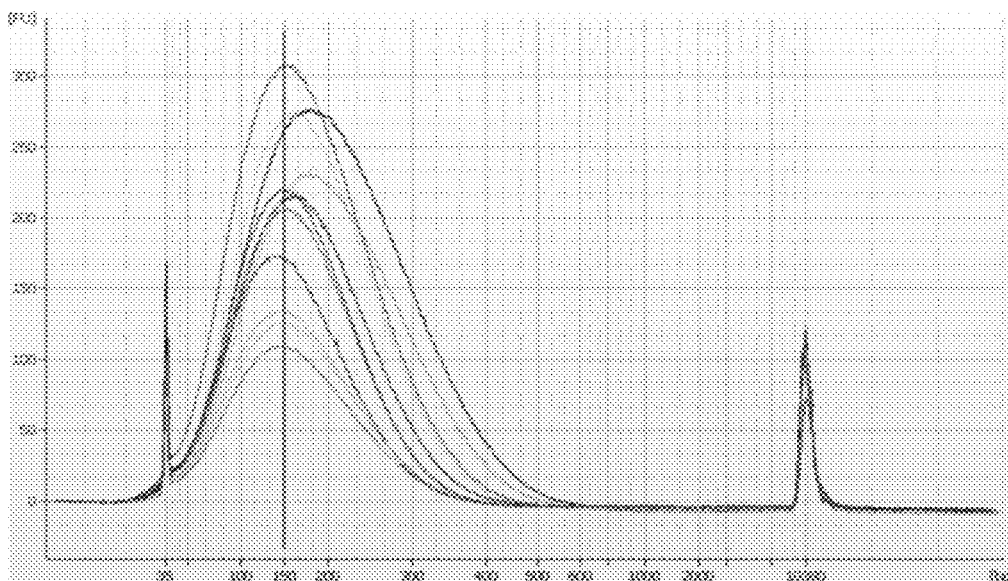


FIG 8A

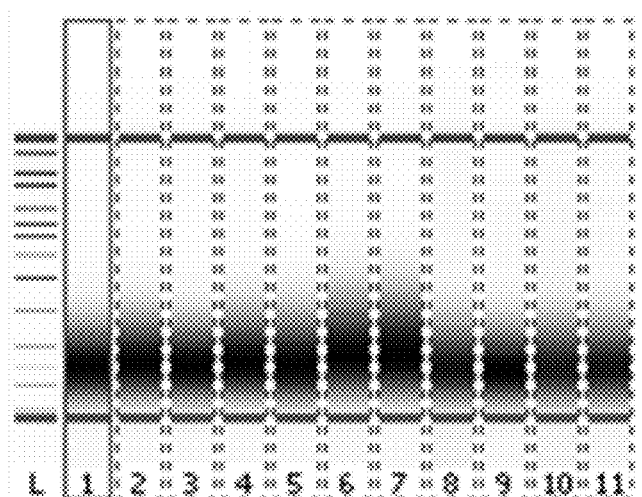


FIG 8B

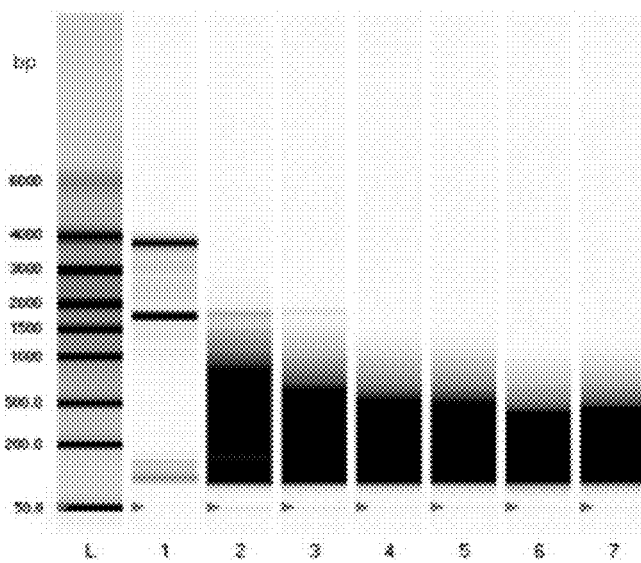


FIG 9A

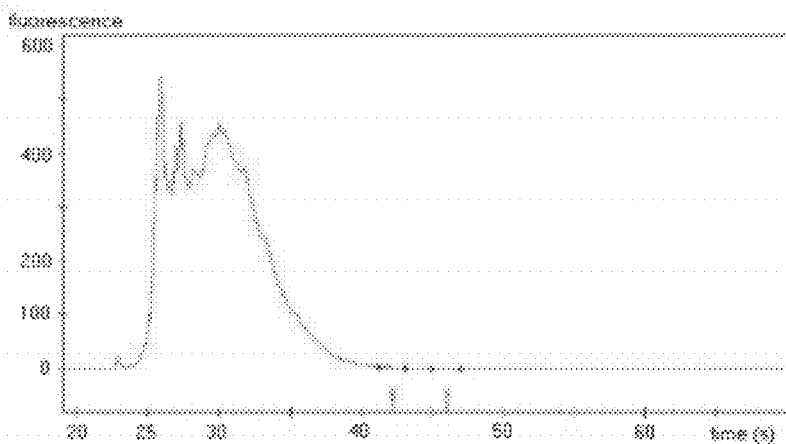


FIG 9B

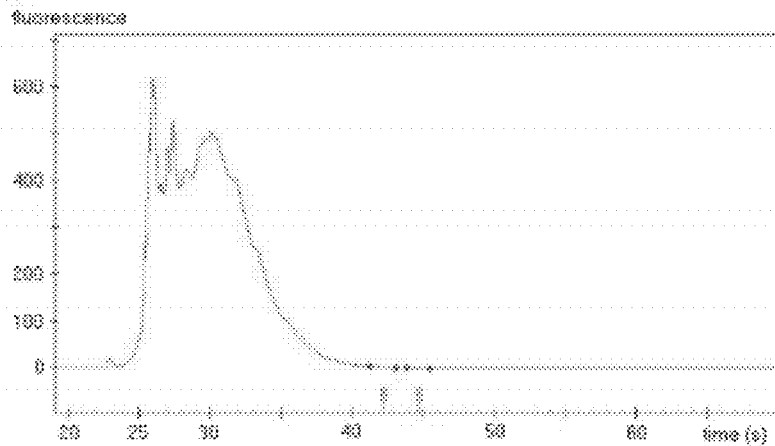


FIG 9C

FRAGMENTING DNA SEQUENCES LONGER THAN 10,000 BP USING ULTRASONICATION

RELATED APPLICATIONS

This application claims the priority benefit under 35 U.S.C. §119 of European Application No. 11162716.2, filed on Apr. 14, 2011, which is incorporated herein by reference in its entirety.

The present invention relates to methods and apparatuses for fragmentation of DNA, in order to fragment a larger DNA sequence into sequence fragments of smaller size. In particular, the present invention relates to the fragmentation of DNA by shearing using ultrasound waves, also referred to as sonication.

It has long been known to use ultrasound for creating focused mechanical stress to rupture cell walls, e.g. from GB 1363934 and U.S. Pat. No. 4,874,137. The ultrasound waves pass through the sample, expanding and contracting liquid. During expansion, molecules are pulled away from one another and cavities or bubbles are formed in a process called cavitation. The bubble continues to absorb energy until it can no longer sustain itself and then implodes, producing intense focused shearing forces, which rupture cell walls.

It is also known to use 20 kHz ultrasound waves for fragmenting DNA, which frequency is believed to provide for shorter treatment times (Mann T L, Krull U J, "The application of ultrasound as a rapid method to provide DNA fragments suitable for detection by DNA biosensors", *Biosensors and Bioelectronics*, Vol. 20, 2004, pp. 945-955; Rageh M. M., El-Lakkani A., et al., "Effect of high power ultrasound on aqueous solution of DNA", *International Journal of Physical Sciences*, Vol. 4, 2009, pp. 63-68).

Other apparatuses work with much higher frequencies in the MHz range (see e.g. U.S. Pat. No. 6,719,449).

Apparatuses for ultrasound shearing are known to be configured to perform different kinds of operations (cell lysis, DNA shearing, chromatin shearing). For each application, a number of specific usage protocols have been determined. These may include selecting the size of the sample, the periodicity of activation of the ultrasound waves and duty cycle, and the total duration of treatment.

One apparatus suitable for DNA fragmentation by ultrasound is commercialised by the Assignee under the name Bioruptor® (Diagenode, Belgium). Samples of DNA or chromatin are suspended in a liquid solution in a sample tube. The sample tube is suspended in a tank filled with a liquid medium (typically water). Ultrasound wave transducers are coupled to the bottom wall of the tank. Upon activation of the transducers, ultrasound waves having a frequency of 20 kHz are generated at the bottom wall of the tank, and propagate through the liquid medium to the sample tube. From the sample tube, the ultrasound waves are transmitted to its content, which then experiences mechanical stresses as indicated above. In the DNA sequence fragments, the double stranded (ds) DNA recovery is low.

In an article entitled "Specificity of DNA Cleavage by Ultrasound", *Molecular Biology*, 2006, Vol. 40 No. 2, pp. 276-283, Grokhovsky analyses cleavage of DNA fragments having a starting size of 439-475 bp in 0.2 ml sample tubes at a concentration of 5-10 µg/ml using ultrasound at 44 kHz and 22 kHz, but does not see any effect between the two frequencies.

In an article entitled "Development of a fast and efficient ultrasonic-based strategy for DNA fragmentation", *Talanta* 81 (2010), pp. 881-886, Larginho et al evaluate several

ultrasound-based platforms for DNA sample preparation. They found that a device referred to as the Sonoreactor UTR200, Heilscher Ultrasound Tech working at 24 kHz showed the best efficiency of DNA fragmentation and was considered the best ultrasonic tool to achieve effective DNA fragmentation at high throughput. An ultrasonic bath was found to have a low intensity of sonication with consequently a cavitation efficiency which is insufficient for promoting considerable DNA fragmentation.

Document WO 93/03150 concerns DNA fragmentation using a frequency of 60 kHz. The document describes to perform the ultrasonic treatment similar to what is explained in EP 0337690. In the latter document, ultrasound treatment is effected based on application of an ultrasonic tip to the wall of a cuvette.

Since fragmented DNA is increasingly being used in the preparation of sequencing libraries, there is an increased need of providing DNA fragments of predetermined size and with as little variance (spread) on the size as possible. Due to the increasing demand for fragmented DNA, there also exists a need of improving the cost-effectiveness of DNA fragmentation, and hence increasing the useable fraction of the fragmented DNA and increasing throughput times of DNA fragmentation processes by reducing fragmentation time.

The present invention therefore aims to provide methods and apparatuses that allow to obviate drawbacks of the prior art.

In particular, it is an aim of the invention to provide methods and apparatuses enabling to fragment DNA so that fragments with a small variance/standard deviation in size are obtained.

It is an aim of the invention to provide methods and apparatuses enabling to fragment RNA as well.

It is also an aim of the invention to provide methods and apparatuses which enable to improve the cost-effectiveness of fragmenting DNA.

It is also an aim of the invention to provide methods and apparatuses which enable to decrease the time needed for fragmenting DNA and increase the throughput.

It is also an aim of the invention to provide methods and apparatuses which enable to augment dsDNA recovery in DNA sequence fragments.

According to an aspect of the invention, there is provided a method of fragmenting a DNA sequence into fragments of smaller size as set out in the appended claims. The DNA sequence is suspended in a solution, which can be liquid or gel-like, and is subjected to the action of ultrasound waves so as to shear the DNA.

According to the invention, the ultrasound waves have a frequency as indicated in the appended claims. The inventors found that using such a frequency enables to obtain smaller size distributions for the obtained fragments, to reduce the time required for obtaining such fragments and to use lower ultrasound power intensities for shearing as compared to the known frequency of about 20 kHz. This results not only in an increased usefulness of DNA shearing methods of the invention for sequencing applications, but also allows reducing costs.

Further aspects of the invention are set out in the appended dependent claims.

According to another aspect of the invention, there is provided an apparatus for use in methods of the invention, as set out in the appended claims.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 represents an apparatus for DNA shearing using ultrasound waves according to the invention.

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FIG. 2 represents a plot of intermittent (cyclic) generation of ultrasound waves.

FIG. 3 represents a graph of the size distribution of DNA sequence fragments as obtained in example 1 described below. Size distribution (in base-pair) is plotted versus Fluorescence Units (FU).

FIG. 4 represents a graph of the mean size variation between different runs (under same conditions) of DNA sequence fragments obtained with example 2, for three different treatment durations (A: 15 minutes, B: 40 minutes, C: 60 minutes). Y-axis corresponds to the size of DNA fragments in base pair.

FIG. 5A-C represents comparative electropherograms of DNA fragments obtained after sonication at 40 kHz and at 20 kHz as described in Example 4.

FIGS. 6A-C represent agarose gel electrophoresis results of sonicated samples comprising DNA fragments in differing concentrations according to Example 5. Each figure (A-C) shows results of different runs.

FIG. 7 represents an electropherogram of 11 out of the 12 samples of FIG. 6A.

FIGS. 8A-B represent electrophoresis results of DNA fragmentation in samples of 50 μ l and 100 μ l volume in accordance with Example 6.

FIGS. 9A-C represent electrophoresis results of total RNA fragmentation according to the invention. FIG. 9A represents a gel electrophoresis of total RNA dissolved in 100 μ l samples and sonicated for a varying duration as indicated in Example 7. FIG. 9B shows an electropherogram corresponding to lane 4 of FIG. 9A. FIG. 9C shows an electropherogram corresponding to lane 5 of FIG. 9A.

DETAILED DESCRIPTION OF THE INVENTION

Aspects of the invention relate to the fragmentation of DNA sequence into DNA sequence fragments of smaller size. The starting material is genomic or plasmid DNA, or DNA with a size larger than or equal to 10000 base pair (bp), advantageously larger than or equal to 25000 bp.

Aspects of the invention relate equally to fragmentation of RNA sequence into RNA sequence fragments. It will be convenient to note that where in the present description fragmentation of DNA sequences are described, same methods and apparatuses are understood to apply to RNA fragmentation as well.

Methods of the invention are arranged to fragment such sequence into fragments having a mean size smaller than or equal to 5000 bp, preferably smaller than or equal to 2000 bp, preferably smaller than or equal to 1300 bp, preferably smaller than or equal to 1075 bp, preferably smaller than or equal to 800 bp, preferably smaller than or equal to 400 bp, preferably smaller than or equal to 275 bp, preferably smaller than or equal to 175 bp. The mean size of the obtained sequence fragments is preferably larger than or equal to 50 bp, preferably larger than or equal to 100 bp. Indicated upper and lower size limits can be combined to yield optimal size ranges.

Fragmentation is effected by shearing using ultrasound waves. According to an aspect of the invention, ultrasound waves having a frequency larger than or equal to about 28 kHz, advantageously larger than or equal to about 32 kHz, advantageously larger than or equal to about 35 kHz, advantageously larger than or equal to about 36 kHz advantageously larger than or equal to 37 kHz, and smaller than or equal to about 80 kHz, advantageously smaller than or equal to about 60 kHz, advantageously smaller than or equal to

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about 50 kHz, advantageously smaller than or equal to about 48 kHz, advantageously smaller than or equal to about 45 kHz and advantageously smaller than or equal to about 43 kHz are used. Indicated upper and lower frequency limits can be combined to yield optimal frequency ranges.

Alternatively, ultrasound waves having a frequency larger than or equal to about 45 kHz, advantageously larger than or equal to about 49 kHz, and smaller than or equal to about 80 kHz, advantageously smaller than or equal to about 60 kHz can be used, wherein indicated upper and lower frequency limits can be combined.

Such ultrasound waves can be generated by known transducers, such as piezoelectric or magnetostrictive transducers. Excitation of the DNA sequence by the ultrasound waves is advantageously indirect, in that the ultrasound waves are generated at a remote location and are made to propagate through one or more media before arriving at the sequence. Indirect excitation can cause a gentler excitation of the sequence, so that more consistent fragments are obtained.

Referring to FIG. 1, there is provided an apparatus 10 capable of subjecting a DNA sequence-comprising solution to ultrasound waves in accordance with aspects of the present invention. Such a solution can be liquid or gel-like as is known in the art. The apparatus of FIG. 10 is constructionally similar to apparatuses as described in U.S. Pat. No. 4,874,137, which reference is incorporated herein by reference.

In apparatus 10, the DNA sequence-comprising solution (sample) is provided in a container, preferably a sample tube 11.

Container 11 and the solution are excited indirectly by the ultrasound waves. The apparatus therefore comprises a main body 12 which holds a tank 13 configured for containing a liquid, preferably water. Container 11 keeps the solution isolated from the medium (water) within the tank 13.

The tank 13 may be closed by a lid 14 which is configured for keeping the sample tube 11 suspended in the tank 13.

One or more ultrasound wave generators (transducers) 15 are coupled externally to the tank 13, preferably underneath the bottom of tank 13. Transducers 15 can be of the magnetostrictive type and are configured to generate mechanical vibrations, having a frequency as indicated, and which are transmitted to the tank 13. For operation, tank 13 is filled with a liquid. A drain pipe 21 may be provided to drain the liquid from tank 13 after operation. The mechanical vibrations of the tank 13 propagate through the liquid in the form of pressure (ultrasound) waves of same frequency.

In operation, the sample tube 11 is suspended (or bathed) in the liquid within tank 13, so that the tube 11 is subjected to the action of the ultrasound (pressure) waves propagating through the liquid and vibrates.

Sample tubes made of polypropylene, polymethylpentene or polycarbonate can be used. It has been observed that a sample tube made of polypropylene gives better results.

It is preferred that the sample tube 11 is so suspended in the liquid of tank 13 that the liquid level of the DNA sequence-comprising solution in sample tube 11 is lower than the level of the liquid in tank 13.

Preferably, sample tubes 11 tapering towards the bottom end are used. The sample tubes 11 are advantageously sized to contain a maximal volume larger than or equal to about 0.1 ml, advantageously larger than or equal to about 0.25 ml, advantageously larger than or equal to about 0.4 ml. The sample tube size is advantageously smaller than or equal to about 10 ml, advantageously smaller than or equal to about

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5 ml, advantageously smaller than or equal to about 2 ml, advantageously smaller than or equal to about 1 ml.

Transducers **15** are electrically connectable to a control and power supply unit **16**, which can be configured for controlling the frequency of excitation, the power, duration and any other settable parameter relating to the generation of the ultrasound waves.

Control unit **16** is advantageously provided with a human interface panel, on which one or more of the above indicated parameters can be set. By way of example, control unit **16** can be provided with a control knob **161** for setting the output power of the generated ultrasound waves. The output power may be visualized on an intensity level indicator **162**. Transducers **15** advantageously have a total (input) power in the range between about 10 W and about 350 W, advantageously between about 10 W and about 200 W. This corresponds to a power intensity (in the liquid of tank **13**) of between about 0.25 W/m² and about 8.75 W/m², advantageously between about 0.25 W/m² and about 5 W/m². It is to be noted that there is a significant difference between the theoretical power delivered by the transducer and the actual power dissipated in the liquid in tank **13**, see A. W. Davis and D. R. Phillips, "A Defined Molecular-Weight Distribution of Deoxyribonucleic Acid after Extensive Sonication", *Biochem. J.* (1978) 173, pp. 179-183).

Control unit **16** and/or transducers **15** may be configured to generate ultrasound waves of a single fixed frequency, not selectable by an operator.

The duration of treatment can be set with a timer **163**. Possible durations fall in the range between about 30 s and about 100 minutes, advantageously between about 30 s and about 60 minutes. The duration refers to the total time of treatment, including non-active periods in case of intermittent (cyclic) operation.

In addition, the control unit can be provided with a selector **164** for selecting intermittent generation of ultrasound waves. Transducers **15** can be configured to operate intermittently, such as in (equal) cycles formed of an active period (Ta) wherein the transducers are active and generate ultrasound waves and an inactive period (Ti) wherein the transducers are not active and do not generate ultrasound waves, as illustrated in FIG. 2.

The sum of the active and inactive time periods within a single cycle is referred to as the cycle period Tc. The ratio of active period Ta to the cycle period Tc is referred to as the duty cycle.

Possible cycle periods are longer than or equal to about 2 s, advantageously longer than or equal to about 4 s, advantageously longer than or equal to about 8 s. They may be shorter than or equal to about 6 minutes (360 s), advantageously shorter than or equal to about 3 minutes (180 s), advantageously shorter than or equal to about 2 minutes (120 s). Possible duty cycles fall in the range between about 0.1 (10%) and about 0.8 (80%), advantageously between about 0.2 and about 0.7, advantageously between about 0.3 and about 0.7.

DNA Total cycle number may vary between 1 and 100.

Advantageously, a holder **171** for simultaneously suspending a plurality of sample tubes **11** from lid **14** can be provided. This has the advantage that a plurality of DNA sequence samples can be treated (fragmented) simultaneously, which increases throughput. Holder **171** can be connected to a gear wheel **172** for coupling to a motor **18** enabling to rotate the holder **171** during operation.

Main body **12** is advantageously placed in a soundproof box **19** for acoustic isolation. Box **19** can be provided with a closing soundproof lid **191**.

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For optimized treatment, the solution should preferably be maintained at temperatures between about 4° C. and about 10° C., even during treatment. Since ultrasound excitation causes a temperature increase, apparatus **10** preferably comprises a temperature control unit (cooling unit) **20** configured for maintaining the solution at a predetermined temperature. One way of effecting temperature control is to keep the liquid of tank **13** cooled, as illustrated in FIG. 1.

Apparatuses as described hereinabove can be advantageously used to carry out methods of the invention. In order to carry out such methods, the starting sequence should be suitably conditioned. This can comprise an extraction and purification step of the DNA sequence from a biological sample containing DNA, such as a cell or a tissue and dissolving the obtained DNA sequence in a sonication buffer, such as a TE buffer (Tris-EDTA buffer) having a pH in the range between about 7.5 and about 8.0. Other conditioning steps, such as adding to the DNA-containing solution a solid support, an organic solution, a detergent, a positively charged polymer, or organic molecules may be of interest.

The DNA concentration in the sonication buffer advantageously falls in the range between about 0.001 µg/µl and about 0.5 µg/µl, advantageously between about 0.001 µg/µl and about 0.25 µg/µl, advantageously between about 0.001 µg/µl and about 0.1 µg/µl.

Of the DNA sequence-containing solution, a volume advantageously smaller than or equal to 500 µl, advantageously smaller than or equal to 400 µl, advantageously smaller than or equal to 300 µl, advantageously smaller than or equal to 250 µl, advantageously smaller than or equal to 150 µl is put in a container, such as a sample tube **11**, which can have sizes as indicated. A volume of DNA sequence-containing solution of at least 1 µl is advantageously used, advantageously at least 10 µl.

The container with isolated volume of DNA sequence-containing solution is then subjected to the action of ultrasound waves of frequency as indicated.

One or more protocols may be set up for carrying out shearing/fragmenting treatment according to the invention in order to obtain DNA sequence fragments of desired (mean) size, such as mean sizes as indicated hereinabove and with narrow size distributions. Methods of the invention enable to fragment the DNA sequence into fragments of smaller size and having a size distribution with a coefficient of variance advantageously smaller than 15%, advantageously smaller than 12%.

The protocol may include a selection of the frequency of the ultrasound waves. Frequency may be dependent on (or determined by) the apparatus used.

The protocol may include a selection of the power or energy intensity of the ultrasound waves.

The protocol may include a selection of the duration of the treatment and/or periodicity (intermittent or continuous) of the treatment. Preferred values for duration and periodicity are as indicated hereinabove.

Methods of the invention can be used with any type of double stranded DNA can be used, from plasmid DNA or synthetic dsDNA to large genomic DNA. The DNA can be obtained from various species such as Human, Mouse, Rat, Loris (Strepsirrhine primate), Lemur, Chimpanzee, *Xenopus laevis*, bacteria such as *E. coli*, yeast, etc.

DNA fragments as obtained through methods of the invention are advantageously used for the creation of genomic libraries for further DNA sequencing applications. Therefore, the method and apparatus according to the invention can be combined with complementary DNA sequencing

methods and apparatus. DNA fragments as obtained through methods of the invention may as well find application in adapting material properties, such as in polymers and carbon nanotubes.

EXAMPLE 1

DNA Fragmentation at 38.5-41.5 kHz

Sample preparation: For each test sample, 1 µg human genomic DNA (Coriell Cell Repositories, NA 18507) was dissolved in 100 µl TE buffer (10 mM Tris, 1 mM EDTA, pH 8.0). A volume of 100 µl of the solution was put in a Costar® 0.65 ml Low Binding Microcentrifuge Tube (Cat. no. 3206). The sample is vortexed gently during 10 sec and then centrifuged for 10 sec to collect the sample at the bottom of the tube before being subjected to ultrasound waves.

Setup: an apparatus as represented in FIG. 1 is used, having a tank filled with about 750 ml of water. The sample tube with DNA buffer is placed in a holder and suspended in the water, such that the buffer level in the sample tube lies below the water level in the tank. The water in the tank is maintained at 4° C. using a cooling unit. Magnetostrictive transducers are coupled to the bottom of the tank and are configured for oscillating at 40 kHz±1.5 kHz (measured at 38.5-41.5 kHz) with total (input) power of about 150W. Transducers were activated intermittently using cycles of 10 s ON/30 s OFF or 30 s ON/30 s OFF (indicated for each test result).

treatment duration is required for obtaining DNA fragments of smaller size. Also evident from table 1 is the high dsDNA recovery in DNA sequence fragments, for example: about 90% dsDNA recovery for DNA sequence fragments of about 1000 bp and about 50% dsDNA recovery for DNA sequence fragments of about 100 bp. The dsDNA was quantified using an intercalating dye exhibiting a higher specificity for double stranded DNA, for example SYBR® Green dye. Longer sonication times (i.e. higher treatment duration) induce more degradation of ds DNA and generate smaller fragments, more single stranded (ss) DNA and more single strand breaks. The lower the power and/or the lower the treatment duration, the higher the percentage of dsDNA recovery in the DNA sequence fragments.

EXAMPLE 2

Run-to-Run Variation

FIG. 4 plots the run-to-run variation of the average size of sheared DNA fragments obtained with three experiments with same settings and duration of treatment in same apparatus as in example 1 (A: 15 minutes, B: 40 minutes, C: 60 minutes total duration). Standard conditions were used in each case (30 s/30 s cycles (50% duty cycle), Low power setting or 150 W), human Genomic DNA (Cell Repositories, NA18507), 0.65 ml sample tubes. Samples were analysed on Bioanalyzer 2100 with High Sensitivity DNA chips.

TABLE 1

Example 1 test results (bp = base pair, SD = standard deviation, CV = coefficient of variation (%), ' = minutes).											
No.	cycles	Mean size (bp)			peak width at 1/2 height		peak width at 1/4 height		double-stranded DNA recovery (%)		
		mean	SD	CV	Max	Min	Max	Min	mean	SD	CV
1	2 cycles 10/30	1230	67.3	5.7	1179	720	1562	903	91.3	2.5	2.7
2	3 cycles 10/30	1038	32.8	3.4	1588	493	1387	683	95.4	8.7	9.1
3	4 cycles 10/30	848	49.7	5.9	1240	455	1078	619	89.4	2.3	2.5
4	2' 30/30	676	77.4	10.7	953	402	832	517	85.5	2.5	2.9
5	3' 30/30	476	33.4	7.2	635	311	564	393	82.2	4.0	4.8
6	5' 30/30	319	27.6	8.7	426	211	373	270	81	4.9	6.0
7	7' 30/30	234	23.4	9.1	323	150	272	188	76.1	5.5	7.2
8	10' 30/30	200	11.1	5.2	277	121	236	165	73.4	5.8	7.9
9	15' 30/30	183	10.5	5.7	207	98	179	126	67.1	5.5	8.2
10	40' 30/30	135	5.2	3.9	171	86	151	111	52.7	8.0	15.3
11	60' 30/30	115	5.0	4.5	151	77	134	97	48.1	5.3	13.9

All test results are analysed using an Agilent 2100 Bio-analyzer with High Sensitivity DNA chip.

Eleven test samples (referenced with consecutive Arabic numerals) were exposed to ultrasound waves as indicated, but under different cycle conditions (number of cycles, duration). Obtained test results are summarized in table 1 and are plotted in FIG. 3. As is evident from table 1, a longer

COMPARATIVE EXAMPLE 3

DNA Fragmentation at 20 kHz and 40 kHz

Table 2 shows comparative data of sonication time required for fragmenting a same starting DNA sequence into fragments of indicated target size. It can be clearly deduced

from the table that the reduction in sonication time is more significant for smaller fragment sizes (at least 50% reduction in sonication time for fragments of 700 bp or smaller).

TABLE 2

Comparative data for effective sonication time (total active sonication time, excluding inactive periods) for fragmenting a DNA sequence into a target fragment size		
Target size	Total sonication (active time only) time at 40 kHz	Total sonication (active time only) time at 20 kHz
150 bp	15 min	45 min
200 bp	6 min 30 s	30 min
350 bp	2 min 15 s	5 min
450 bp	1 min 30 s	3 min
700 bp	1 min	2 min
900 bp	45 s	1 min
1250 bp	20 s	30 s

COMPARATIVE EXAMPLE 4

DNA Fragmentation at 20 kHz and 40 kHz

To compare the DNA shearing efficiency at the two frequencies, samples were prepared under the following conditions. An apparatus as used in example 1 is used for the 40 kHz experiments. An apparatus with similar construction, but producing 20 kHz ultrasound waves is used for the 20 kHz experiments. In both cases, a 12×0.65-ml sample tube holder was used for maintaining 0.65 ml Low Binding tubes (Costar, Ref. 3206) in the water bath. Human genomic DNA was used as template and samples are prepared as in Example 1, but now with a TE buffer of 7.6 pH. The starting size of the DNA fragments in the samples was larger than 50000 bp. All samples were analyzed on a Bioanalyzer 2100 using DNA High Sensitivity chip (1 µl loaded per sample).

The samples were loaded in the apparatuses and ultrasound treatment was performed at maximum power (150 W) using 30 s On-30 s Off cycles (cycle duration 1 minute, duty cycle 0.5). Sonication time was selected in function of to-obtain fragment size

FIGS. 5 A-C show a comparison of the obtained DNA size distributions after sonication. FIG. 5A compares obtained fragment sizes of 200 bp mean size. Methods and apparatuses of the invention only require 10 minutes of total sonication treatment to obtain DNA fragments of 200 bp, whereas at 20 kHz one would need 30 minutes to obtain fragments of same size. This means a time saving of 20 minutes or 66% compared to prior art procedures.

FIG. 5B compares obtained fragment sizes of 135 bp mean size. Methods and apparatuses of the invention only require 20 minutes of total sonication treatment to obtain DNA fragments of 135 bp, whereas at 20 kHz one would need 60 minutes to obtain fragments of same size. This means a time saving of 40 minutes or 66% compared to prior art procedures.

FIG. 5C compares obtained fragment sizes of 115 bp mean size. Methods and apparatuses of the invention only require 40 minutes of total sonication treatment to obtain DNA fragments of 115 bp, whereas at 20 kHz one would need 80 to 100 minutes to obtain fragments of same size. This means a time saving of 50% and more compared to prior art procedures.

EXAMPLE 5

Impact of DNA Sample Concentration on Sonication Performance

In the present experiment the influence of DNA concentration in the test samples subjected to sonication was tested. A same sonication apparatus as used in example 1 (and described with reference to FIG. 1) and configured to generate 40 kHz ultrasound waves was used. The water bath was maintained at 4° C. It was equipped with a 12×0.65-ml tube holder, holding 0.65 ml Low Binding sample tubes (Costar, Ref. 3206).

Human genomic DNA (starting concentration: 0.373 µg/µl, source: Coriell Cell Repositories) was used as template for preparing the samples. Samples with three different DNA fragment concentrations (0.2 µg/100 µl, 1 µg/100 µl, and 5 µg/100 µl) were prepared in a TE buffer (pH 7.6) solution. All samples had a same volume of 100 µl, and each sample was put in a 0.65 ml sample tube. The starting size of the DNA in the samples was higher than 50000 bp.

Four samples were sonicated per experiment (of same DNA concentration). Each experiment was repeated three times for each concentration and consisted in subjecting the samples to 40 cycles 30 s On, 30 s Off (40 min sonication, 50% duty cycle).

The fragmented DNA samples were analyzed on 1% agarose or on a Bioanalyzer 2100 High Sensitivity DNA chip and the results are shown in FIG. 6A-C for 15 µl of sheared DNA loaded on 1% agarose gel (MW ladder—Small Size). FIG. 6 A shows results of the first run for each concentration. FIGS. 6 B and C show results of the second and third runs respectively for same concentrations.

The results shown in FIG. 6A are represented in the electropherogram of FIG. 7 as well. FIG. 7 shows 11 out of the 12 samples represented in FIG. 6A and was obtained by loading 1 µl of each sheared sample on the Bioanalyzer High Sensitivity DNA. The target DNA fragment size after sonication was 150 base pair. The observed average peak size was 142 bp with a CV=8.9%. The results hence were seen to correlate with the expected target size irrespective of the DNA concentration of the samples. Therefore, fragmentation methods according to the invention work equally well for samples with DNA concentration in the tested range between 0.2 µg and 5 µg/100 µl final volume.

EXAMPLE 6

Impact of Sample Volume on DNA Fragmentation Performance

Experiments were carried out with sample tubes filled with different quantities of DNA solutions. Experiments were carried out in a same apparatus as for Example 5, having a 12×0.65-ml tube holder. 0.65 ml Low Binding sample tubes (Costar, Ref. 3206) were used for the experiments.

Human genomic DNA (starting concentration: 0.204 µg/µl, source: Promega) was used as template for preparing the samples. Samples were prepared based on a TE buffer of pH 7.6. First samples were prepared with a DNA concentration of 0.03 µg/µl and a final sample volume of 50 µl. Second samples were prepared with a DNA concentration of 0.01 µg/µl and a final sample volume of 100 µl. Each sample was put in a 0.65 ml sample tube as indicated above. The starting size of the DNA sequence in the samples was higher than 50000 bp.

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A total of 12 samples (6 of 50 μ l and 6 of 100 μ l) were prepared and subjected to sonication under same conditions as indicated in Example 5 (40 cycles, 30 s On, 30 Off). The samples were analyzed by loading 1 μ l on a Bioanalyzer High Sensitivity DNA chip after sonication treatment. FIG. 8A-B show electrophoresis results for 11 out of the 12 samples. The target size was 150 base pair. The observed average peak sizes correlate very well with the expected target size irrespective of the sample volume used. The 50 μ l sample volumes had an average fragment size of 159.7 bp with CV=8.3%; the 100 μ l sample volume had an average fragment size of 145 bp with CV=2.54%. This means that sample volume variations do not negatively affect performance of methods of the invention.

RNA Fragmentation

EXAMPLE 7

Methods of the invention can also be used for fragmenting RNA sequences in same manner as with DNA sequences as described above. Experiments were conducted with total RNA sequences which were dissolved in a TE buffer (10 mM Tris, 1 mM EDTA, pH 7.5-8.0) which was RNase free. Samples of dissolved RNA were prepared in volumes of 100 μ l with a RNA concentration of 0.05 μ g/ μ l, which were put in 0.65 ml sample tubes. The RNA sequences had a starting size larger than 50000 bp. Same sample tubes and apparatus as with Examples 5 and 6 above were used.

The samples were briefly vortexed and centrifuged for 10 s before starting sonication. In addition, short centrifugation steps after every five sonication cycles were performed. Sonication was performed with 30 s On/30 s Off-cycles at high power (150 W). Total number of cycles depended on target RNA fragment size. The samples were subsequently analysed on Biorad Experion using Eukaryote Total RNA HighSens chip. Results are presented in FIG. 9, showing different RNA size distributions produced by varying the duration of sonication.

FIG. 9A shows duplicate profiles produced after 5 minutes (5 cycles) (lanes 2-3), 10 minutes (10 cycles) (lanes 4-5) and 15 minutes (15 cycles) (lanes 6-7) of sonication. Lane 1 shows the unfragmented total RNA (starting material). Lane L: Internal Molecular Weight Marker.

FIG. 9B-C compares the RNA size distributions of sheared total RNA of lanes 4 and 5 of FIG. 9A respectively. It can be seen that reproducibility of methods of the invention for fragmenting RNA is excellent.

The invention claimed is:

1. A method of fragmenting a DNA sequence having a size of at least 10000 base pair (bp) into fragments having a mean size between 100 bp and 400 bp with a coefficient of variation (CV) between 2.5% and 9.1%, the method comprising:

adding the DNA sequence to a buffer solution at a pH between 7.5 and 8.0 to obtain a solution comprising the DNA sequence, wherein the solution comprising the DNA sequence is put in a container;

placing the container in a liquid bath; and

subjecting the container in the liquid bath to the action of ultrasound waves such that the ultrasound waves travel through the liquid bath to excite the container and the solution comprising the DNA sequence so as to shear the DNA sequence, and wherein the ultrasound waves have a frequency falling in the range between 28 kHz and 80 kHz.

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2. The method of claim 1, wherein the ultrasound waves have a frequency falling in the range between 36 and 50 kHz.

3. The method of claim 1, wherein the ultrasound waves have a frequency falling in the range between 36 and 43 kHz.

4. The method of claim 1, wherein the solution comprising the DNA sequence has a volume smaller than or equal to 500 μ l.

5. The method of claim 1, wherein the solution comprising the DNA sequence has a DNA concentration falling in the range between 0.001 μ g/ μ l and 0.5 μ g/ μ l.

6. The method of claim 1, wherein the solution comprising the DNA sequence has a DNA concentration falling in the range between 0.001 μ g/ μ l and 0.1 μ g/ μ l.

7. The method of claim 1, wherein the solution comprising the DNA sequence is subjected intermittently to the ultrasound waves.

8. The method of claim 7, wherein the ultrasound waves are generated in cycles having a duration between 2 s and 360 s and a duty cycle between 10% and 80%.

9. The method of claim 1, wherein the container is a low binding, tube sized to contain a maximal volume between 0.1 ml and 10 ml.

10. The method of claim 1, wherein the container comprises multiple containers that are positioned at different locations in the liquid bath.

11. The method of claim 10, wherein the multiple containers are held in a support which is rotated relative to the liquid bath.

12. The method of claim 1 further comprising cooling the solution during application of the ultrasound waves.

13. The method of claim 1, wherein the liquid bath is contained in a tank and ultrasound transducers are externally coupled to the tank, and wherein subjecting the container in the liquid bath to the ultrasound waves is performed through excitation of the tank.

14. A method of fragmenting a DNA sequence having a size of at least 10000 base pair (bp) into fragments having a mean size between 400 bp and 800 bp with a coefficient of variation between 7.2% and 10.7%, the method comprising: adding the DNA sequence to a buffer solution at a pH between 7.5 and 8.0 to obtain a solution comprising the DNA sequence wherein the solution comprising the DNA sequence is put in a container;

placing the container in a liquid bath; and

subjecting the container in the liquid bath to the action of ultrasound waves such that the ultrasound waves travel through the liquid bath to excite the container and the solution comprising the DNA sequence so as to shear the DNA sequence, and wherein the ultrasound waves have a frequency falling in the range between 28 kHz and 80 kHz.

15. A method of fragmenting a DNA sequence having a size of at least 10000 base pair (bp) into fragments having a mean size between 800 bp and 1300 bp with a coefficient of variation between 3.4% and 5.9%, the method comprising:

adding the DNA sequence to a buffer solution at a pH between 7.5 and 8.0 to obtain a solution comprising the DNA sequence, wherein the solution comprising the DNA sequence is put in a container;

placing the container in a liquid bath; and

subjecting the container in the liquid bath to the action of ultrasound waves such that the ultrasound waves travel through the liquid bath to excite the container and the solution comprising the DNA sequence so as to shear

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the DNA sequence, and wherein the ultrasound waves have a frequency falling in the range between 28 kHz and 80 kHz.

16. The method of claim **14**, wherein the container is a low binding tube sized to contain a maximal volume between 0.1 ml and 10 ml. 5

17. The method of claim **15**, wherein the container is a low binding tube sized to contain a maximal volume between 0.1 ml and 10 ml.

18. The method of claim **14**, wherein the ultrasound waves have a frequency falling in the range between 36 and 50 kHz. 10

19. The method of claim **15**, wherein the ultrasound waves have a frequency falling in the range between 36 and 50 kHz. 15

20. The method of claim **14**, wherein the liquid bath is contained in a tank and ultrasound transducers are externally coupled to the tank, and wherein subjecting the container in the liquid bath to the ultrasound waves is performed through excitation of the tank. 20

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